



OIPE

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/09/627,896B

TIME: 13:12:30

Input Set : A:\08702.0081-01000 seq listing as filed.txt

Output Set: N:\CRF4\03192003\I627896B.raw

3 <110> APPLICANT: CO, MAN SUNG
 4 VASQUEZ, MAXIMILIANO
 5 CARRENO, BEATRIZ
 6 CELNIKER, ABBIE CHERYL
 7 COLLINS, MARY
 8 GOLDMAN, SAMUEL
 9 GRAY, GARY S.
 10 KNIGHT, ANDREA
 11 O'HARA, DENISE
 12 RUP, BONITA
 13 VELDMAN, GEERTRUIDA M.
 15 <120> TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
 16 OF TREATMENT THEREWITH
 18 <130> FILE REFERENCE: 08702.0081-01000
 20 <140> CURRENT APPLICATION NUMBER: 09/627,896B
 C--> 21 <141> CURRENT FILING DATE: 2003-03-11
 23 <160> NUMBER OF SEQ ID NOS: 32
 25 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

714 <210> SEQ ID NO: 22
 715 <211> LENGTH: 239
 716 <212> TYPE: PRT
 717 <213> ORGANISM: Mus sp.
 718 <223> OTHER INFORMATION: 3D1 light chain
 E--> 720 <400> SEQUENCE: 22

721	Met	Asp	Ser	Gln	Ala	Gln	Val	Leu	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser
722	1				5					10					15	
724	Gly	Thr	Cys	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala
725				20					25					30		
727	Val	Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser
728			35					40					45			
730	Leu	Leu	Asn	Ser	Arg	Thr	Arg	Glu	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln
731		50					55				60					
733	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg
734	65				70				75						80	
736	Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
737				85					90					95		
739	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr
740			100					105					110			
743	Tyr	Cys	Ser	Gln	Ser	Tyr	Asn	Leu	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys

*<220> insert this revised identifier
 wherever <221>, <222>
 or <223> is
 shown*

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```

744      115      120      125
746 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
747      130      135      140
749 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
750 145      150      155      160
752 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
753      165      170      175
755 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
756      180      185      190
758 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Ser Lys
759      195      200      205
761 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
762      210      215      220
764 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
765 225      230      235

```

1081 <210> SEQ ID NO: 25

1082 <211> LENGTH: 327

1083 <212> TYPE: DNA

1084 <213> ORGANISM: Homo sapiens

1085 <223> OTHER INFORMATION: III2R light chain variable region

E--> 1087 <400> SEQUENCE: 25

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1088 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
1090 atcacttgcc gggcgagtc gggcattagc aattatttag cctggtatca gcagaaacca      120
1092 gggaaagttc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct      180
1094 cggttcagtg gcagtggatc tgggacagat ttcactctca ccatacagcag cctgcagcct      240
1096 gaagatgttg caacttatta ctgtcaaaag tataacagtg cccctccgag tacgttcggc      300
1098 caagggacca aggtggaaat caaacgt                                327

```

1101 <210> SEQ ID NO: 26

1102 <211> LENGTH: 339

1103 <212> TYPE: DNA

1104 <213> ORGANISM: Homo sapiens

1105 <223> OTHER INFORMATION: H2F light chain variable region

E--> 1107 <400> SEQUENCE: 26

```

1108 gacatccagt tgaccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc      60
1110 atcaactgca agtccagcca gagtgtttta tacagctcca acaacaagaa ttacttaact      120
1112 tggatccagg agaaaccagg acagcctcct aagctgctca tttactgggc atctaccggg      180
1114 gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc      240
1116 atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact      300
1118 cctcgaacgt tcggccaagg gaccaaggtg gaaatcaaa                                339

```

1121 <210> SEQ ID NO: 27

1122 <211> LENGTH: 95

1123 <212> TYPE: PRT

1124 <213> ORGANISM: Homo sapiens

1125 <223> OTHER INFORMATION: III2R light chain variable region

E--> 1127 <400> SEQUENCE: 27

```

1129 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1130 1      5      10      15
1132 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
1133      20      25      30

```

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Input Set : A:\08702.0081-01000 seq listing as filed.txt

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1135 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
 1136 35 40 45
 1138 Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 1139 50 55 60
 1141 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 1142 65 70 75 80
 1144 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro
 1145 85 90 95

1148 <210> SEQ ID NO: 28

1149 <211> LENGTH: 101

1150 <212> TYPE: PRT

1151 <213> ORGANISM: Homo sapiens

1152 <223> OTHER INFORMATION: H2F light chain variable region

E--> 1154 <400> SEQUENCE: 28

1156 Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1157 1 5 10 15
 1159 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 1160 20 25 30
 1162 Ser Asn Asn Lys Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro
 1163 35 40 45
 1165 Pro Lys Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 1166 50 55 60
 1168 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 1169 65 70 75 80
 1172 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 1173 85 90 95

1175 Tyr Tyr Ser Thr Pro

1176 100

1179 <210> SEQ ID NO: 29

1180 <211> LENGTH: 368

1181 <212> TYPE: DNA

1182 <213> ORGANISM: Homo sapiens

1183 <223> OTHER INFORMATION: III2R heavy chain variable region

E--> 1185 <400> SEQUENCE: 29

1186 aggtgcagct ggtgcagtct ggggctgagg tgaagaagcc tgggtcctcg gtaaaggctc 60
 1188 cctgcaaggc ttctggaggc accttcagta gttatactat cagctgggtg cgacaggccc 120
 1190 ctggacaagg gcttgagtgg atgggaagga tcatgcctat ccttggaacta gcaaattacg 180
 1192 cacagaagtt ccagggcaga gtcacgatta ccgcggacaa atccacgagc acagcctaca 240
 1194 tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg agagatcccg 300
 1196 attatgtttg ggggagcgac aactggttcg acccctgggg ccagggaacc ctgctcatcg 360
 1198 tctcctca 368

1201 <210> SEQ ID NO: 30

1202 <211> LENGTH: 358

1203 <212> TYPE: DNA

1204 <213> ORGANISM: Homo sapiens

1205 <223> OTHER INFORMATION: H2F heavy chain variable region

E--> 1207 <400> SEQUENCE: 30

1208 gtgcagctgg tggagtctgg gggaggcttg gtcaagcctg gagggctcct gagactctcc 60
 1210 tgtgcagcct cggattcacc ttactagga atcctacgag ctgggtacgc caggctccag 120

RAW SEQUENCE LISTING

DATE: 03/19/2003

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Input Set : A:\08702.0081-01000 seq listing as filed.txt

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```

1212 ggaaggggct ggagtggttg gttaatataa tggtagtcgg aattgaacca tactatgcgg      180
1214 actctgtgaa gggccgattc accatctcca gaggcaacgc caagaactca ctgtatctgc      240
1216 aaatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcgaga gggatctgtc      300
1218 ttatgacaga ggctactttg actactgggg ccaggggaacc ctggtcaccg tctcctca      358

```

1221 <210> SEQ ID NO: 31

1222 <211> LENGTH: 97

1223 <212> TYPE: PRT

1224 <213> ORGANISM: Homo sapiens

1225 <223> OTHER INFORMATION: III2R heavy chain variable region

E--> 1227 <400> SEQUENCE: 31

```

1229 Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser
1230 1 5 10 15
1233 Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Thr
1234 20 25 30
1237 Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1238 35 40 45
1241 Arg Ile Met Pro Ile Leu Gly Leu Ala Asn Tyr Ala Gln Lys Phe Gln
1242 50 55 60
1245 Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met
1246 65 70 75 80
1249 Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
1250 85 90 95
1253 Arg

```

1257 <210> SEQ ID NO: 32

1258 <211> LENGTH: 98

1259 <212> TYPE: PRT

1260 <213> ORGANISM: Homo sapiens

1261 <223> OTHER INFORMATION: H2F heavy chain variable region

E--> 1263 <400> SEQUENCE: 32

```

1265 Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
1266 1 5 10 15
1269 Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Tyr
1270 20 25 30
1273 Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1274 35 40 45
1277 Tyr Ile Ser Ser Arg Gly Ser Glu Thr Ile Tyr Tyr Ala Asp Ser Val
1278 50 55 60
1281 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
1282 65 70 75 80
1285 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
1286 85 90 95
1289 Ala Arg

```

E--> 1291 ??

E--> 1293 ??

E--> 1294 (...continued)

E--> 1296 (continued...)

VERIFICATION SUMMARY

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Input Set : A:\08702.0081-01000 seq listing as filed.txt

Output Set: N:\CRF4\03192003\I627896B.raw

L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:720 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:22
L:881 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 23
L:1087 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:25
L:1107 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:26
L:1127 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:27
L:1154 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:28
L:1185 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:29
L:1207 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:30
L:1227 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:31
L:1263 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:32
L:1291 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:1291 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1291 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
M:332 Repeated in SeqNo=32
L:1293 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1293 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1294 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1294 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1296 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1296 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1296 M:252 E: No. of Seq. differs, <211> LENGTH:Input:98 Found:100 SEQ:32